

GenCore version 4.5  
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OK protein - protein search, using sw model

Run on: January 7, 2002, 16:03:53 ; Search time 180.87 Seconds

(without alignments)  
37,201 Million cell updates/sec

Title: US-08-569-749-7

Perfect score: 269  
Sequence: 1 LARAGFYITGPGDRVACFAC.....MEPKDAMSEHRRHPNCPF 46

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPREMBL.17:\*  
2: sp.archaea:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.rodent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	248	92.2	1140	4 Q9UNH1	Q9unh1 homo sapien
2	243	90.3	589	11 Q9QZC6	Q9qzc6 rattus norv
3	243	90.3	589	11 Q9ESB8	Q9ese8 rattus norv
4	236	87.7	602	11 Q9SES9	Q9ese9 rattus norv
5	228	84.8	195	13 Q9IA70	Q9ia70 gallus gall
6	228	84.8	197	13 Q9IA69	Q9ia69 gallus gall
7	228	84.8	224	11 Q98642	Q98642 rattus norv
8	228	84.8	324	13 Q9PDN2	Q9pdn2 gallus gall
9	228	84.8	610	13 Q57319	Q57319 gallus gall
10	185	68.8	466	11 Q9ESR0	Q9esr0 rattus norv
11	185	68.8	501	11 Q9EQ05	Q9eq05 rattus norv
12	185	68.8	501	11 Q9EQ05	Q9eq05 rattus norv
13	141	52.4	597	11 Q9R015	Q9r015 mus musculu
14	133.5	49.6	4845	11 Q98738	Q98738 mus musculu
15	132.5	49.3	153	5 Q9YEM2	Q9yem2 dirosophila
16	129	48.0	264	12 Q9YEM2	Q9yem2 dirosophila
17	129	48.0	438	5 Q9YUX5	Q9yux5 dirosophila
18	127	47.2	280	4 Q9HAP7	Q9hap7 homo sapien
19	127	47.2	298	4 Q9H2A8	Q9h2a8 homo sapien

20	126	46.8	261	12 Q9SES9	Q9ses9 epiphyas po
21	126	46.8	379	5 Q9U492	Q9u492 trichoplusi
22	125	46.5	276	12 Q98744	Q98744 buzura supp
23	123	45.7	268	12 Q9E232	Q9e232 helioverpa
24	123	45.7	268	12 Q9IF18	Q9if18 helioverpa
25	123	45.7	281	12 Q9YNL8	Q9ynl8 choristoneu
26	123	45.7	313	12 Q9J827	Q9j827 spodoptera
27	123	45.7	377	5 Q9N107	Q9n107 spodoptera
28	117	42.9	208	12 Q55770	Q55770 chilo iride
29	115.5	42.9	4904	5 Q9VH01	Q9vh01 dirosophila
30	111	41.3	150	12 Q9YV4	Q9yv4 dirosophila
31	107	39.8	155	12 Q9YMI9	Q9ymi9 lymantria d
32	101.5	37.7	142	6 Q9GLN5	Q9gln5 sus scrofa
33	99.5	37.0	142	13 Q9DDK0	Q9ddk0 gallus gall
34	98	36.4	292	12 Q92394	Q92394 bombyx mori
35	97	36.1	281	12 Q9DV15	Q9dvt5 pluteia xy
36	92	34.2	284	12 Q9YKL5	Q9ykl5 epiphyas po
37	87.5	32.5	187	12 Q9DSW8	Q9dsw8 ascovirus d
38	85.5	31.8	285	12 Q9PYQ9	Q9pyq9 xestia c-ni
39	80	29.7	249	12 Q92435	Q92435 bombyx mori
40	80	29.7	301	12 Q9P254	Q9p254 trichoplusi
41	72	26.8	155	5 Q92837	Q92837 caenorhabdi
42	72	26.8	317	12 Q9B649	Q9b649 spodoptera
43	70.5	26.2	137	4 Q9BV24	Q9bv24 homo sapien
44	66.5	24.7	329	12 Q9YVX0	Q9yvxo metanoplus
45	65	24.2	87	11 Q09119	Q09119 mus musculu

## ALIGNMENTS

RESULT 1  
ID Q9UNH1 PRELIMINARY; PRT: 1140 AA.  
AC Q9UNH1;  
DT 01-MAY-2000 (TREMBLrel, 13, Created)  
DT 01-MAY-2000 (TREMBLrel, 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel, 17, Last annotation update)  
DE AP12-MLT FUSION PROTEIN.  
GN AP12-MLT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99272400; PubMed=10339464;  
RA Dietlamm J., Baens M., Wlodarska I., Stefanova-Ouzounova M.,  
RA Hernandez J.M., Hossfeld D.K., De Wolf-Peters C., Hagemeijer A.,  
RA Van den Bergh H., Marynen P.;  
RT "The apoptosis inhibitor gene AP12 and a novel 18q gene, MLT, are  
RT recurrently rearranged in the t(11;18)(q21;q21)pesassociated with  
RT mucosa-associated lymphoid tissue lymphomas";  
RL Blood 93:3601-3609(1999).  
CC EMBL: AF123094; AAD46161.1; -;  
CC HSSP: Q13490; IOBH.  
DR InterPro: IPR001370; BIR.  
DR InterPro: IPR003576; Caspase.  
DR InterPro: IPR001309; ICE\_p20.  
DR InterPro: IPR003598; IG\_C2.  
DR InterPro: IPR003600; IG\_Like.  
DR InterPro: IPR003006; IG\_MHC.  
DR Pfam: PF00653; BIR\_3.  
DR Pfam: PF00647; Ig\_2.  
DR SMART: SM00238; BIR\_3.  
DR SMART: SM00115; CASC\_1.  
DR SMART: SM00408; IC2\_1.  
DR SMART: SM00410; IC\_Like\_1.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
DR PROSITE: PS50208; CASPASE\_P20; 1.

SEQ SEQUENCE 1140 AA: 128738 MW: 0C18D890287C723E CRC64;

Query Match 92.2%; Score 248; DB 4; Length 1140;  
Best Local Similarity 91.3%; Pred. No. 3.3e-23;  
Matches 42; Conservative 2; Mismatches 0; Gaps 0;

OY 1 LARAGFYIIGPDGVACFCAGCGKLSNMEPKDAMSEHRHPPNCPF 46  
1199 LAKAGFYITGPDGVACFCAGCGKLSNMEPKDAMSEHRHPPNCPF 234

RESULT 2

ID 09QZC6 PRELIMINARY; PRT: 589 AA.

AC 09QZC6 01-MAR-2001 (TREMBLrel. 13, Created)  
DT 01-MAR-2001 (TREMBLrel. 13, Last sequence update)  
DE INHIBITOR OF APOPTOSIS PROTEIN 2.

OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;

RN 11

RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY;  
RA Dong 2., Denton M., Gu S.M., Saikumar P., Venkatchalam M.A.,  
RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2.";  
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.

CC -1 SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.

DR EMBL: AF190020; AAF04585.1; "

DR HSSP: Q13490; 1QBH.

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001315; CARD.

DR InterPro: IPR001841; znf\_fing.

DR Pfam: PF00653; BIR: 3.

DR Pfam: PF00619; CARD: 1.

DR Pfam: PF00097; zf-C3HC4; 1.

DR SMART: SM00238; BIR: 3.

DR SMART: SM00114; CARD: 1.

DR SMART: SM00184; RING: 1.

DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.

DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.

DR PROSITE: PS50209; CARD: 1.

DR Zinc-finger.

SO SEQUENCE 589 AA: 66777 MW: E6812FE3EA34142 CRC64;

Query Match 90.3%; Score 243; DB 11; Length 589;  
Best Local Similarity 87.0%; Pred. No. 7.4e-23;  
Matches 40; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDGVACFCAGCGKLSNMEPKDAMSEHRHPPNCPF 46  
1199 LAKAGFYITGPDGVACFCAGCGKLSNMEPKDAMSEHRHPPNCPF 221

RESULT 3

ID 09SESE8 PRELIMINARY; PRT: 589 AA.

AC 09SESE8 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DE INHIBITOR OF APOPTOSIS PROTEIN 2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN 11

RP SEQUENCE FROM N.A.

RA Holcik M., Lefevre C.A., Hicks K., Korneluk R.G.;

RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of  
Apoptosis Protein 1, 2, and 3 Genes.";  
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.

CC -1 SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.

DR EMBL: AF183431; AAG22970.1; "

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001315; CARD.

DR InterPro: IPR001841; znf\_fing.

DR Pfam: PF00653; BIR: 3.

DR Pfam: PF00619; CARD: 1.

DR Pfam: PF00097; zf-C3HC4; 1.

DR SMART: SM00238; BIR: 3.

DR SMART: SM00114; CARD: 1.

DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.

DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.

DR PROSITE: PS50209; CARD: 1.

DR Zinc-finger.

SO SEQUENCE 589 AA: 66750 MW: B4F7089BD7CD285B CRC64;

Query Match 90.3%; Score 243; DB 11; Length 589;  
Best Local Similarity 87.0%; Pred. No. 7.4e-23;  
Matches 40; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDGVACFCAGCGKLSNMEPKDAMSEHRHPPNCPF 46  
1199 LAKAGFYITGPDGVACFCAGCGKLSNMEPKDAMSEHRHPPNCPF 221

RESULT 4

ID 09SESE9 PRELIMINARY; PRT: 602 AA.

AC 09SESE9 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DE INHIBITOR OF APOPTOSIS PROTEIN 1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN 11

RP SEQUENCE FROM N.A.

RA Holcik M., Lefevre C.A., Hicks K., Korneluk R.G.;

RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of

Apoptosis Protein 1, 2, and 3 Genes.";

RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.

CC -1 SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.

DR EMBL: AF183430; AAG22970.1; "

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001315; CARD.

DR InterPro: IPR001841; znf\_fing.

DR Pfam: PF00653; BIR: 3.

DR Pfam: PF00619; CARD: 1.

DR Pfam: PF00097; zf-C3HC4; 1.

DR SMART: SM00238; BIR: 3.

DR SMART: SM00114; CARD: 1.

DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.

DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.

DR PROSITE: PS50209; CARD: 1.

DR Zinc-finger.

SO SEQUENCE 602 AA: 67326 MW: CC913855EA62DE5A CRC64;

Query Match 87.7%; Score 236; DB 11; Length 602;  
Best Local Similarity 84.8%; Pred. No. 5.9e-22;  
Matches 39; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDGVACFCAGCGKLSNMEPKDAMSEHRHPPNCPF 46  
1199 LAKAGFYITGPDGVACFCAGCGKLSNMEPKDAMSEHRHPPNCPF 234

	RESULT	5	PRT:	195 AA.
ID	G9IA70			
AC	G9IA70:			
Dt	01-OCT-2000 (TREMBLrel. 15, Created)			
Dt	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
Dt	01-JUN-2001 (TREMBLrel. 17, last annotation update)			
De	INHIBITOR OF APOPTOSIS 1 (FRAGMENT).			
Ox	Gallus gallus (Chicken).			
Cc	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Ancroauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
CC	Gallus.			
OX	NCHI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRED LEHORN; TISSUE=SPLLEN;			
RA	Zhou H., Lamont S.J.;			
FT	"Genetic variation among chicken lines and mammalian species in			
RT	specific genes".			
RL	Submitted(JAN-2000) to the EMBL/genbank/DDBJ databases.			
DR	EMBL: AF221082, AAC53519.1; ..			
Dr	IInterPro: IPR001370; BIR.			
DR	PIfam: PF00653; BIR: 2.			
DR	SMART: SM00238; BIR: 2,			
DR	PROSITE: PS01282; BIR_REPEAT_1: 2.			
DT	PROSITE: PS50143; BIR_REPEAT_2: 2.			
FT	NON_TER	1		
FT	NON TER	195		
SQ	SEQUENCE	195 AA; 22347 MW; 9C39BFA75E2AE48 CRC64;		
	Query Match	84.8%; Score 228; DB 13; Length 195;		
	Best Local Similarity	80.4%; Pled No. 2e+21; Mismatches 4; Indels 0;		
MATCHES	37; Conservative	5; Gaps 0;		
OY	1 LAAGFYITGEGDKVACFACGGCLSNWEPKDXMSHRHFPCPF 46			
DB	50 LAAKLGYTGTADRVACTGCGLSNWEPKDAMSEHRHFPCPFCR 95			
RESULT	6			
ID	G9IA69			
AC	G9IA69:			
Dt	01-OCT-2000 (TREMBLrel. 15, Created)			
Dt	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
Dt	01-JUN-2001 (TREMBLrel. 17, last annotation update)			
De	INHIBITOR OF APOPTOSIS 1 (FRAGMENT).			
Ox	Gallus gallus (Chicken).			
Cc	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Ancroauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
CC	Gallus.			
OX	NCHI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRED FAYOUMI; TISSUE=SPLEEN;			
RA	Zhou H., Lamont S.J.;			
FT	"Genetic variation among chicken lines and mammalian species in			
RT	specific genes".			
RL	Submitted(JAN-2000) to the EMBL/genbank/DDBJ databases.			
DR	EMBL: AF221083; AAC53520.1; ..			
Dr	IInterPro: IPR001370; BIR.			
DR	PIfam: PF00653; BIR: 2.			
DR	SMART: SM00238; BIR_REPEAT_1: 2.			
DR	PROSITE: PS50143; BIR_REPEAT_2: 2.			
FT	NON_TER	1		
FT	NON TER	197		
SQ	SEQUENCE	197 AA; 22602 MW; D7923DABC623BE1A CRC64;		

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QY      1 LARAGFYIIGPDNRVACFACGKLSNWEKKDANSEHRRHPNCPP 46
        ||||| | 1:|||| |:||||| ||||| ||||| ||||| |||||
DB      105 LGKAIFYTGGDRVPCFCAGCGKLSNWBNDLSEHRHRFPNCP 150

RESULT      7
O9DDN2      PRELIMINARY; PRT; 224 AA.
AC          O88642:
DT          01-NOV-1998 (TREMBLrel.. 08, Created)
DT          01-NOV-1998 (TREMBLrel.. 08, Last sequence update)
DT          01-JUN-2001 (TREMBLrel.. 17, Last annotation update)
DE          INHIBITOR OF APOPTOSIS PROTEIN (FRAGMENT).
GN          RIAP1.
OS          Rattus norvegicus (Rat).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN          [1]
RP          NCBJ_TaxID=10116;
RC          SEQUENCE FROM N.A.
RA          STRAIN=WISTAR; TISSUE=OVARY; CORPUS LUTEUM;
RA          Bradley C.K., Lareu R.R., Dharmarajan A.M.;
RT          "Cloning and characterisation of an inhibitor of apoptosis protein
RT          (RIAP) in the rat corpus luteum."
RL          Submitted (AUG-1998) to the EMBL/GenBank/DDAJ databases.
DR          HSSP: AF081503; AAC32497.1; -.
DR          HSSP: O13490; IOBH.
DR          InterPro: IPR001370; BIR.
DR          Pfam: PF006653; BIR_2.
DR          SMART: SMO0238; BIR: 2.
FT          POSITIVE: PS50143; BIR_REPEAT_2; 3.
FT          NON_TER 1
FT          NON_TER 224
SQ          SEQUENCE 224 AA; 25209 MW; 213A52534D5B56A CRC64;

Query Match      84.8%; Score 228; DB 11; Length 224;
Best Local Similarity 80.4%; Pred. No. 2e-21;
Matches 37; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 LARAGFYIIGPDNRVACFACGKLSNWEKKDANSEHRRHPNCPP 46
        ||||| | 1:|||| |:||||| ||||| ||||| ||||| |||||
DB      105 LGKAIFYTGGDRVPCFCAGCGKLSNWBNDLSEHRHRFPNCP 150

RESULT      8
O9DDN2      PRELIMINARY; PRT; 324 AA.
AC          O9DDN2:
DT          01-MAR-2001 (TREMBLrel.. 16, Created)
DT          01-MAR-2001 (TREMBLrel.. 16, Last sequence update)
DT          01-JUN-2001 (TREMBLrel.. 17, last annotation update)
DE          APOPTOSIS INHIBITOR CH-1AP1 (FRAGMENT).
OS          Gallus gallus (Chicken).
OC          Archyonta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Eukaryota; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC          Gallus
OX          NCBI_TaxID=9031;
RN          [1]
RP          SEQUENCE FROM N.A.
RA          Hendrickson C.N., Bergmann W.J., Varadarajan J., Rose H.R. Jr.;
RT          "The apocytosis inhibitor ch-1ap1 is a direct transcriptional target of
RT          v-rel and c-rel."
RL          Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR          EMBL: AF311289; AAC42316.1; -.
DR          InterPro: IPR001370; BIR.
DR          Pfam: PF006653; BIR: 3.
DR          SMART: SMO0238; BIR: 3.
FT          POSITIVE: PS01282; BIR_REPEAT_1; 1.
FT          NON_TER 1
FT          NON_TER 324
SQ          SEQUENCE 324 AA; 35209 MW; 213A52534D5B56A CRC64;
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DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
 FT NON\_TER 324 324  
 SEQUENCE 324 AA: 36567 MW: 58289DENE3733P3 CRC64;

Query Match 84.8%; Score 228; DB 13; Length 324;  
 Best Local Similarity 80.4%; Pred. No. 3,3e-21;  
 Matches 37; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFCAGKLSNWEPRKDNAMSEHRRHPNCPF 46  
 DB 196 LAKAGLYLTGADKACVCTCGQLSNWEPRKDNAMSEHRRHPNCPF 241

RESULT 9  
 ID 057319 PRELIMINARY; PRT; 610 AA.  
 AC 057319.  
 DT 01-JUN-1998 (TREMURel. 06, Created)  
 DT 01-JUN-1998 (TREMURel. 06, last sequence update)  
 DT 01-JUN-2001 (TREMURel. 17, last annotation update)  
 DE INHIBITOR OF APOPTOSIS PROTEIN 1 (IAP) (INHIBITOR OF T CELL APOPTOSIS PROTEIN).  
 GN IAP.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-WHITE LEGHORN; TISSUE-EMBRYONIC FIBROBLAST;  
 RX MEDLINE-9803801; PubMed-9372964;  
 RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;  
 RT "ch-IAP, a member of the inhibitor-of-apoptosis protein family, is a mediator of the antiapoptotic activity of the v-Rel oncoprotein.",  
 RT Mol. Cell. Biol. 17:7328-7341(1997)  
 CC -1- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED CELLS.  
 CC -1- SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF THE V-REL-TRANSFORMED CELLS.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE SPLEEN, THYMUS, BURSAS, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS IN TESTIS, BRAIN, AND SKELETAL MUSCLE.  
 CC -1- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION PROCESS.  
 CC -1- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.  
 CC -1- SIMILARITY: MEMBER OF THE IAP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF APOPTOSIS PROTEIN REPEAT).  
 CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.  
 DR EMBL: AF008592; AAB88044.1; -;  
 DR HSBP: Q13490; 10BH.  
 DR InterPro: IPR001370; BIR.  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR001841; ZnF\_ring.  
 DR Pfam: PF00653; BIR\_3.  
 DR Pfam: PF00619; CARD\_1.  
 DR Pfam: PF00097; ZF-C3HC4\_1.  
 DR SMART: SM00238; BIR\_3.  
 DR SMART: SM00114; CARD\_1.  
 DR SMART: SM00184; RING\_1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
 DR PROSITE: PS50209; CARD; 1.  
 KW Apoptosis; zinc-finger; Repeat.  
 FT REPEAT 30 97 BIR\_REPEAT 1.  
 FT REPEAT 176 242 BIR\_REPEAT 2.  
 FT REPEAT 262 329 BIR\_REPEAT 3.  
 FT ZN\_FING 563 597 C3HC4-TYPE.  
 FT SEQUENCE 610 AA: 68924 MW: 46P4761950B44A6 CRC64;

Query Match 84.8%; Score 228; DB 13; Length 610;  
 Best Local Similarity 80.4%; Pred. No. 6,2e-21;  
 Matches 37; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFCAGKLSNWEPRKDNAMSEHRRHPNCPF 46  
 DB 196 LAKAGLYLTGADKACVCTCGQLSNWEPRKDNAMSEHRRHPNCPF 241

RESULT 10  
 ID 09E005 PRELIMINARY; PRT; 496 AA.  
 AC 09E005.  
 DT 01-MAR-2001 (TREMURel. 16, Created)  
 DT 01-MAR-2001 (TREMURel. 16, last sequence update)  
 DT 01-JUN-2001 (TREMURel. 17, last annotation update)  
 DE INHIBITOR OF APOPTOSIS PROTEIN 3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;  
 RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of Apoptosis Protein 1, 2, and 3 Genes."  
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.  
 DR EMBL: AF183429; AAG22969.1; -;  
 DR InterPro: IPR001370; BIR.  
 DR InterPro: IPR001841; ZnF\_ring.  
 DR Pfam: PF00653; BIR\_3.  
 DR Pfam: PF00097; ZF-C3HC4\_1.  
 DR SMART: SM00238; BIR\_3.  
 DR SMART: SM00114; CARD\_1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
 KM Zinc-finger.  
 SQ SEQUENCE 496 AA: 56117 MW: 98E142AAEC5B798 CRC64;

Query Match 68.8%; Score 185; DB 11; Length 496;  
 Best Local Similarity 71.7%; Pred. No. 1,5e-15;  
 Matches 33; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFCAGKLSNWEPRKDNAMSEHRRHPNCPF 46  
 DB 184 LASAGLYLTGIDGVCCGKLSNWEPRKDNAMSEHRRHPNCPF 229

RESULT 11  
 ID 09E005 PRELIMINARY; PRT; 501 AA.  
 AC 09E005.  
 DT 01-MAR-2001 (TREMURel. 16, Created)  
 DT 01-MAR-2001 (TREMURel. 16, last sequence update)  
 DT 01-JUN-2001 (TREMURel. 17, last annotation update)  
 DE INHIBITOR OF APOPTOSIS PROTEIN 3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-WISTAR; TISSUE-OVARY;  
 RA Lareu R.R., Bradley C.K., Lacher M., Fells R.R., Dharmarajan A.M.;  
 RT "Cloning, characterization and regulation of an inhibitor of apoptosis protein in the rat corpus luteum."  
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.  
 DR EMBL: AF304333; AAC41192.1; -;  
 DR InterPro: IPR001370; BIR.  
 DR InterPro: IPR001841; ZnF\_ring.

DR pfam: PF00653; BIR: 3.  
DR pfam: PF00097; zf-C3HC4; 1.  
DR SMART: SM00238; BIR: 3.  
DR SMART: SM00184; RING; 1.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.  
DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
KW Zinc-finger.  
SQ SEQUENCE 501 AA; 56548 MW; 0973BF28E81C5A0 CRC64;

Query Match 68.8%; Score 185; DB 11; Length 501;  
Best Local Similarity 71.7%; Pred. No. 1.5e-15;  
Matches 33; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

OY 1 LARAGFYIGDGVACGKLSNWKPDAMSEHRRHPNCPF 46  
DB 184 LASAGLYTGIDVQCFCGKLNWPCDRANSEHRRHPNCPF 229

RESULT 12  
O9EO04 PRELIMINARY; PRT; 501 AA.  
AC O9EO04;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE INHIBITOR OF APOPTOSIS PROTEIN 3.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Felis.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MISTAR; TISSUE=OVARY;  
RA Lareu R.R., Bradley C.K., Lacher M., Ellis R.R., Dharmarajan A.M.;  
RT Cloning, characterization and regulation of apoptosis  
RT protein in the rat corpus luteum.  
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.  
CC EMBL: AF04334; AAC41193.1;  
DR InterPro: IPR001370; BIR.  
DR InterPro: IPR001841; Znf\_ring.  
DR pfam: PF00653; BIR: 3.  
DR SMART: SM00238; BIR: 3.  
DR SMART: SM00184; RING; 1.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.  
DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
KW Zinc-finger.  
SQ SEQUENCE 501 AA; 56578 MW; 4863F69FF2E0C8CD CRC64;

Query Match 68.8%; Score 185; DB 11; Length 501;  
Best Local Similarity 71.7%; Pred. No. 1.5e-15;  
Matches 33; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

OY 1 LARAGFYIGDGVACGKLSNWKPDAMSEHRRHPNCPF 46  
DB 184 LASAGLYTGIDVQCFCGKLNWPCDRANSEHRRHPNCPF 229

RESULT 13  
O9RO15 PRELIMINARY; PRT; 597 AA.  
ID O9RO15;  
AC O9RO15;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE NEURONAL APOPTOSIS INHIBITORY PROTEIN.  
GN BIRCIE OR NAIP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=99431676; PubMed=10501978;  
RA Huang S., Schaff J.M., Gromey J.D., Endlitz M.G., Dietrich W.F.;  
RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct  
RT functional transcripts."  
RL Mamm. Genome 10:1032-1035(1999).  
DR EMBL: AF134493; AA056765.1;  
DR HSSP: Q13490; 10BH.  
DR MGD: MGI:1298220; Bircie.  
DR InterPro: IPR001370; BIR.  
DR pfam: PF00653; BIR: 3.  
DR SMART: SM00238; BIR: 3.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; UNKNOWN\_2.  
DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
SQ SEQUENCE 597 AA; 68322 MW; 4042E36E51A7F9A0 CRC64;

Query Match 52.4%; Score 141; DB 11; Length 597;  
Best Local Similarity 52.2%; Pred. No. 7.4e-10;  
Matches 24; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

OY 1 LARAGFYIGDGVACGKLSNWKPDAMSEHRRHPNCPF 46  
DB 135 LSAGCFVFTGKRDVQCFCGSGISGNWEGDDPWKEHAKWPKCF 180

RESULT 14  
O88738 PRELIMINARY; PRT; 4845 AA.  
ID O88738;  
AC O88738;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE UBIQUITIN-CONJUGATING ENZYME.  
GN BIRC6.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=98292517; PubMed=9628897;  
RA Hausser H.P., Bardoff M., Pyrovolakis G., Jentsch S.;  
RT "A giant ubiquitin-conjugating enzyme related to IAP apoptosis  
RT inhibitors".  
RL J. Cell Biol. 141:1415-1422(1998).  
CC -1- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER  
CC PROTEINS (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE - AMP +  
CC PYROPHOSPHATE + PROTEIN N-UBIQUITYLlysine.  
CC -1- PATHWAY: SECOND STEP IN UBIQUITIN CONJUGATION.  
CC -1- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-  
CC THIOLESTER FORMATION (BY SIMILARITY).  
CC -1- SIMILARITY: TO UBIQUITIN-CONJUGATING ENZYMS DOMAIN.  
DR EMBL: Y17267; CAA76720.1;  
DR HSSP: Q13490; 10BH.  
DR MGD: MGI:1276108; Birc6.  
DR InterPro: IPR001370; BIR.  
DR InterPro: IPR00608; UBO\_conjugat.  
DR pfam: PF00653; BIR: 1.  
DR SMART: SM00238; BIR: 1.  
DR SMART: SM00212; UBCG; 1.  
DR PROSITE: PS0143; BIR\_REPEAT\_2; 1.  
DR PROSITE: PS0127; UBIQUITIN\_CONJUGAT\_2; 1.  
KW Lysase: Ubiquitin conjugation.  
SQ SEQUENCE 4845 AA; 528418 MW; 35C585F73B8CF94C CRC64;

Query Match 49.6%; Score 133.5; DB 11; Length 4845;  
Best Local Similarity 51.0%; Pred. No. 5.6e-08;

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Matches 25; Conservative 4; Mismatches 17; Indels 3; Gaps 1;
QY 1 LARAGFYIYIG---ICGDRVACFACGCKLSNWPCKDDAMSEHRRHFPNCPF 46
:|:|:|:|:| 11 11 1 111 1: 111 11 11111
Db 284 MAAGCFYHOPASSGDDRAMCFCTGCVLCWMEPTDEPMSEHERHSNPCEP 332

RESULT 15
QYVEM2 PRELIMINARY: PRT: 153 AA.
ID QYVEM2
AC 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE CG12265 PROTEIN.
GN CG12265
OS Drosophila melanogaster (Fruit fly)
OC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Adiyanti A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaisl M., Jalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
RA Palazzolo M., Plattman K., Sanders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamas I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-T., Wasarman D.A., Weinstock G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003716; AAF55399.1; -
DR HSSP: Q13490; IOBH.
DR FLYBase: FBgn0038489; CG12265.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR. 1.
DR SMART: SM00238; BIR. 1.
DR PROSITE: PSS0143; BIR_REPEAT_2: 1.
SO SEQUENCE 153 AA; 17455 MW; E250E3B669EC359 CRC64;

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Query Match 49.3%; Score 132.5; DB 5; Length 153;
Best local Similarity 46.9%; Pred. No. 2.3e-09;
Matches 23; Conservative 4; Mismatches 19; Indels 3; Gaps 1;
QY 1 LARAGFYIYIG---ICGDRVACFACGCKLSNWPCKDDAMSEHRRHFPNCPF 46
:|:|:|:|:| 11 11 1 111 1: 111 11 11111
Db 51 MAAGCFYHOPASSGDDRAMCFCTGCVLCWMEPTDEPMSEHERHSNPCEP 332

Search completed: January 7, 2002, 16:03:53
Job time: 1412 sec

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